EXHIBIT

2

```
CLUSTAL W (1.82) Multiple Sequence Alignments


Sequence format is Pearson
Sequence 1: SEQIDNO1           488 aa
Sequence 2: SEQIDNO3.          488 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score:   96
Guide tree       file created:    [/ebi/extserv/clustalw-work/interactive/clustalw-2
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences:    2       Score:10380
Alignment Score 2880
CLUSTAL-Alignment file created   [/ebi/extserv/clustalw-work/interactive/clustalw-200
```

CLUSTAL W (1.82) multiple sequence alignment

```
SEQIDNO1     KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV  60
SEQIDNO3.    KEIAVTIDDKNVIASASGSFLGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV  60
             ***************.* ** ***************************************

SEQIDNO1     GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETEDDLVKLTKG  120
SEQIDNO3.    GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTKG  120
             **************************************************** *:*******

SEQIDNO1     SKMRLLFDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS  180
SEQIDNO3.    SKMRLLFDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS  180
             ************************************************************

SEQIDNO1     AHNLTEKQVGEDFKALHKVLEKYPTLNKGSLVGPDVGWMGVSYVKGLADGAGDLVTAFTL  240
SEQIDNO3.    AHNLTEKQVGEDFKALHKVLEKYPTLNKGSLVGPDVGWMGVSXVKGLADEAGDHVTAFTL  240
             ****************************************** ****** *** ******

SEQIDNO1     HQYYFDGNTSDVSTYLDATYFKKLQQLFDKVKDVLKNSQHKDKPLWLGETSSGYNSGTKD  300
SEQIDNO3.    HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDEPLWLGETSSGYNSGTED  300
             ************* *********************** * *** *************** :*

SEQIDNO1     VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV  360
SEQIDNO3.    VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV  360
             ************************************************************

SEQIDNO1     GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDEDVTLKIDQYGG  420
SEQIDNO3.    GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDGDVTLKIGQYSG  420
             *********************************************** ****** **.*

SEQIDNO1     KKIYSYILTPEGGQLTSQKVLLNGKELKLVSDQLPELNANESKTSFTLSPKTFGFFVVSD  480
SEQIDNO3.    KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVSD  480
             **************************:.***********:*********************

SEQIDNO1     ANVEACKK  488
SEQIDNO3.    ANVEACKK  488
             ********
```

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: SEQIDNO3   488 aa
Sequence 2: SEQIDNO5   488 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 97
Guide tree   file created: [/ebi/extserv/clustalw-work/interactive/clustalw-2
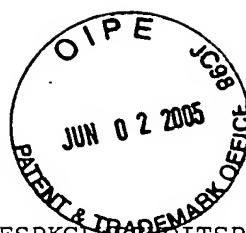Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences: 2   Score:10465
Alignment Score 2927
CLUSTAL-Alignment file created   [/ebi/extserv/clustalw-work/interactive/clustalw-200

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CLUSTAL W (1.82) multiple sequence alignment


SEQIDNO3      KEIAVTIDDKNVIASASGSFLGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV 60
SEQIDNO5      KEIAVTIDDKNVIASASESFHGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV 60
              ******************  **  ************************************


SEQIDNO3      GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTKG 120
SEQIDNO5      GGTFANRLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTKG 120
              ******  ****************************************************


SEQIDNO3      SKMRLLFDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS 180
SEQIDNO5      SKMRLLFDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNGPDHTS 180
              *****************************************************  *****


SEQIDNO3      AHNLTEKQVGEDFKALHKVLEKYPTLNKGSLVGPDVGWMGVSXVKGLADEAGDHVTAFTL 240
SEQIDNO5      AHNLTEKQVGEDFKALHKVLEKYPTLNKGSLVGPDVGWMGVSYVKGLADEAGDHVTAFTL 240
              ****************************************** *****************


SEQIDNO3      HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDEPLWLGETSSGYNSGTED 300
SEQIDNO5      HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDKPLWLGETSSGYNSGTED 300
              ******************************************:*****************


SEQIDNO3      VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV 360
SEQIDNO5      VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYSGYYGPLDKNTLEPNPDYWLMHVHNSLV 360
              ******************************* .****  *********************


SEQIDNO3      GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDGDVTLKIGQYSG 420
SEQIDNO5      GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDEDVTLKIGQYSG 420
              ************************************************ ***********


SEQIDNO3      KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVSD 480
SEQIDNO5      KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPQLNADESKTSFTLSPKTFGFFVVSD 480
              ***********************************:************************


SEQIDNO3      ANVEACKK 488
SEQIDNO5      ANVEACKK 488
              ********
```

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: SEQIDNO3   488 aa
Sequence 2: SEQIDNO7   488 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 94
Guide tree   file created: [/ebi/extserv/clustalw-work/interactive/clustalw-2
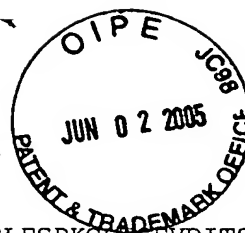Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences: 2   Score:10323
Alignment Score 2848
CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-200

CLUSTAL W (1.82) multiple sequence alignment

```
SEQIDNO3    KEIAVTIDDKNVIASASGSFLGVAFDASLFSPKGLWSFVDITSPKLFKLLEGLSPGYFRV  60
SEQIDNO7    KEIAVTIDDKNVIASVSESFHGVAFDASLFSPKGPWSFVNITSPKLFKLLEGLSPGYFRV  60
            ************** .*  ** ************* ****:*********************

SEQIDNO3    GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDNLVKLTKG  120
SEQIDNO7    GGTFANWLFFDLDENNKWKDYWAFKDKTPETATITRRWLFRKQNNLKKETFDDLVKLTKG  120
            **************************************************:*******

SEQIDNO3    SKMRLLFDLNAEVRTGYEIGKKMTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS  180
SEQIDNO7    SKMRLLFDLNAEVRTGYEIGKKTTSTWDSSEAEKLFKYCVSKGYGDNIDWELGNEPDHTS  180
            ********************** *************************************

SEQIDNO3    AHNLTEKQVGEDFKALHKVLEKYPTLNKGSLVGPDVGWMGVSXVKGLADEAGDHVTAFTL  240
SEQIDNO7    AHNLTEKQVGEDFKALHKVLEKYPTLNKGSPVGPDVGWMGVSYVKGLADGAGDLVTAFTL  240
            ****************************** *********** ****** *** ******

SEQIDNO3    HQYYFDGNTSDVSIYLDATYFKKLQQLFDKVKDVLKDSPHKDEPLWLGETSSGYNSGTED  300
SEQIDNO7    HQYYFDGNTSDVSTYLDASYFKKLQQLFDKVKDVLKNSPHKDKPLWLGETSSGCNSGTKD  300
            ************* ****:*****************:*****:********** ****:*

SEQIDNO3    VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV  360
SEQIDNO7    VSDRYVSGFLTLDKLGLSAANNVKVVIRQTIYNGYYGLLDKNTLEPNPDYWLMHVHNSLV  360
            ************************************************************

SEQIDNO3    GNTVFKVDVSDPTNKARVYAQCTKTNSKHTQSRYYKGSLTIFALNVGDGDVTLKIGQYSG  420
SEQIDNO7    GNTVFKVDVGDPTNKTRVYAQCTKTNSKHTQGKYYKGSLTIFALNVGDEEVTLKIDQYGG  420
            *********.*****:***************.:***************  :*****.**.*

SEQIDNO3    KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVSD  480
SEQIDNO7    KKIYSYILTPEGGQLTSQKVLLNGKELNLVSDQLPELNADESKTSFTLSPKTFGFFVVSD  480
            ************************************************************

SEQIDNO3    ANVEACKK  488
SEQIDNO7    ANVEACKK  488
            ********
```